

ECONOMIC VALUE OF SELECTION FOR RESIDUAL FEED INTAKE IN THE NEW ZEALAND SHEEP INDUSTRY

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SUMMARY

An analysis of the economic benefits and costs of incorporating selection to improve residual feed intake (RFI) in New Zealand's sheep industry was performed. The outcomes indicated that genomic selection for RFI, calibrated on either direct measurement of intake or measurement of greenhouse gases in Portable Accumulation Chambers (PAC) has a positive return when it is assumed that genotyping of candidates in ram breeding flocks is occurring for other traits. A comparison with a hypothetical phenotypic indicator criteria correlated with RFI suggests that further R&D effort is best directed at improving the accuracy of genomic selection in preference to a search for practical indicator measurements.

INTRODUCTION

Feed costs represent a significant component of farm operating costs in New Zealand sheep farming. As such, any reduction in feed costs, while maintaining productivity, may provide an opportunity to increase sheep farming profitability. Genetic improvement is a long-term and sustainable approach to increasing the productivity and profitability of animals, and represents a tool that can be used to improve feed efficiency. This report aims to evaluate the potential benefits from including Residual Feed Intake (RFI) as a criterion in New Zealand sheep breeding programs, and examines 3 alternatives for implementation, being:

1. Genomic selection for RFI calibrated on direct measurement of RFI.
2. Genomic selection for RFI calibrated on indirect measurement of RFI (greenhouse gas production in portable accumulation chambers (PAC)).
3. Phenotype-based selection for RFI based on a hypothetical indicator trait.

MATERIALS AND METHODS

The analysis used standard selection index theory to predict response to selection. A breeding objective was formulated based on models which describe a typical NZ maternal sheep operation. The objective traits included in a standard index include number of lambs born (NLB, Economic weight = 2231c), weaning weight (direct (WWT = 136c) and maternal (WWTM)), carcass weight (CWT = 374c), ewe weight (EWT = -119c), lamb fleece weight (LFW = 261c), hogget fleece weight (HFW = 113c), ewe fleece weight (EFW = 327c), lamb survival (direct (SUR = 8378c) and maternal (SURM)). Three traits were added to this base index, being residual feed intake on growing lambs (RFIL = -112c), replacement hoggets (RFIH = -329), and ewes (RFIE = -495). Genetic correlations between RFI traits were 0.9 (RFIL, RFIH), 0.6 (RFIL, RFIE) and 0.65 (RFIH, RFIE).

A standard group of selection criteria traits formed the base model containing traits commonly used within the Sheep Improvement Ltd genetic evaluation system for NZ sheep industry. These traits included number of lambs born, weaning weight (direct and maternal), carcass weight, hogget fleece weight, survival (direct and maternal), ewe weight, and liveweight at 8 months.

Genomic selection was modeled by including a trait to represent each genomic prediction. The heritability of each genomic trait was set as 0.95, and the accuracy of the prediction was incorporated as a genetic correlation between the genomic prediction and the corresponding profit

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trait. Where other traits were correlated with the corresponding objective trait, the genomic trait was also assumed to be correlated, with the correlation calculated as the accuracy multiplied by the relevant correlation between phenotype traits. Genomic predictors for WWT, WWTM, LW8, LFW, FW12, EFW and NLB were modelled with accuracies of 0.60, 0.45, 0.57, 0.53, 0.32, 0.35, 0.57 respectively. These accuracies were based off the current NZ genomic prediction accuracies (M.Lee, pers. Comm.) weighted by breed representation with the NZ sheep industry.

Accuracy of potential genomic predictions for RFI calibrated from direct measurement, and RFI and Methane Yield calibrated on PAC measurements were modelled based on the equation of Daetwyler et al. (2013). Calibrations were assumed to be against measurements on hoggets. The number of records used in the equation were calculated based on an assumed number of animals measured per year (400 for RFI directly measured and 1400 for PAC measurements) multiplied by the generation interval (3 years) and 5 generations. Effective population size was set at 500 (J. McEwan, Pers Comm) and genome length was 30 Morgans, giving a Me value of 6,279. Sensitivity analysis of assumed accuracies were undertaken (results not shown). Correlations between the calibrated traits and the objective trait RFI_h are given in Table 3, and were multiplied by the accuracy of genomic prediction to give an overall correlation between the genomic prediction and RFI_h. Correlations were extended to RFI_l and RFI_e by multiplying by the relevant correlation with RFI_h. The alternative phenotypic predictor trait for rfi was modelled with a heritability of 0.25 and correlations with RFI objective traits of 0.3. These parameters were considered to be realistic, given that very few candidates for strong physiological indicators of RFI have been discovered in 20 years of significant research on this trait. Table 2 summarises the scenarios modelled.

Table 1. Accuracy of genomic predictions, calculated using equation of Daetwyler *et al* (2013)

	RFI	PAC RFI	PAC_CH4
Genomic accuracy	0.47	0.50	0.62
N records	6,000	21,000	21,000
Heritability	0.30	0.10	0.19
No. measured per year	400	1400	1400
Generation interval	3	3	3
No. Generations	5	5	5
Correlation with RFI _h	1.00	0.57	-0.25

Table 2. Scenarios with different information available. All scenarios included the base phenotypic measurements included as described in the text

Scenario name	Genomics information ¹	Description
Base	N/A	Represents current recording and selection practices (no information available on RFI).
Base+G	growth, reproduction, wool	Represents current recording and selection practices but in which genomic test results are available on selection candidates in industry breeder flocks for a suite of traits (growth, reproduction, and wool), excluding RFI.
Base+G_R	growth, reproduction, wool, RFI	Genomic test results are available on selection candidates in industry breeder flocks for a young animal RFI trait – RFI genomic predictions are calibrated on individual feed intake measures.
Base+G_P	growth, reproduction, wool, PAC_RFI, PAC_CH4	Genomic test results are available on selection candidates in industry breeder flocks for a young animal RFI/CH4 traits calibrated on individual PAC measures.

Base+G_RP	growth, reproduction, wool, RFI, PAC_RFI, PAC_CH4	Genomic test results are available on selection candidates in industry breeder flocks for a young animal RFI trait – RFI genomic predictions are calibrated on both individual feed intake measures and PAC measures.
Base+N	N/A	Represents current recording and selection practices but in which a new phenotypic selection criterion (predictor of feed intake) is available on selection candidates in industry breeder flocks.
Base+NG	growth, reproduction, wool	Represents current recording and selection practices plus genomic test results available on selection candidates in industry breeder flocks for a suite of traits, excluding RFI, and a new selection criterion (predictor of feed intake) is measured on selection candidates in industry breeder flocks.

Calculation of costs and benefits.

Costs were calculated as marginal costs over the cost of recording base phenotypic traits in ram breeding flocks. The cost of genomic selection was calculated based on \$30 per ram tested. Additional costs of including RFI (direct measurement) into the genomic selection was calculated as \$120,000 per year (\$300 per lamb tested), or PAC measurements were \$70,000 per year (\$50 per lamb tested). No additional costs for the implementation of genomic selection were included, as it was assumed that genomic testing was adopted based on the non-RFI traits. The cost of generating industry reference flocks which RFI is measured on was also not included, as these flocks were assumed to be generated for other purposes (e.g. within the current industry progeny test flocks). Cost of the phenotypic indicator trait was \$10 per ram.

Benefits were generated based on the response to selection (in cents per ewe per year). This was then used as an input to a model to portray the flow of rams from breeder flocks and therefore the flow of replacement daughters, genetically improved for RFI, into the national flock (i.e. the number of replacements sired by rams from flocks where RFI was integrated into selection decisions) over time based on a standard flock age structure. The analysis assumes that the first performance recorded offspring will be born with an estimated breeding value/ genomic breeding value for RFI in 2020, the first rams genetically improved for RFI will mate ewes in the commercial flock in 2022, and the first daughters arising from sires genetically improved for RFI will enter the commercial sheep flock as replacements in 2024. There is therefore a two-year lag from generation of genetically improved rams to use in the commercial flock, and a further two-year lag until the daughters of those genetically improved rams enter the commercial flock as replacements. An adoption profile was also included, starting with 20% of rams sourced as being improved for RFI, and increasing by 5% every year to a maximum of 70%. The economic value was calculated as the benefits arising from 10 years of selection, accumulated over 20 years. A discount rate of 7% was used.

RESULTS AND DISCUSSION

Total economic responses across all objective traits are shown in Table 3 along with their relativities to the base and base plus genomics scenarios. Adding genomics to the base scenario led to a 12% increase in gain. Including RFI into the genomic predictions gave an additional 2-6% economic response, depending on the calibration used. Response in RFI traits was greatest in scenarios where genomic calibrations were based on direct measurement of RFI, as might be expected given the assumed correlations of calibration traits with the objective traits. Measurement of a phenotypic predictor of RFI in ram breeding flocks produced approximately 2% additional economic response.

A comparison between costs and benefits shows that the case for inclusion of genomics (excluding RFI) in industry breeding programmes is compelling. Given this, the additional cost of generating specific calibrations for RFI as a hard to measure trait is relatively small compared to the additional benefits gained, and so this analysis supports this model as an implementation pathway for inclusion of RFI into industry breeding programmes. Cost:benefit ration might be

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improved by implementing two-stage selection and reducing costs by only testing the top proportion of rams. Sensitivity results on the accuracy of the genomic predictions (not shown) indicated that there is significant upside to more accurate genomic predictions for RFI. Thus effort into increasing the accuracy is warranted, and under a scenario where one-step genomic evaluation is implemented this would mean: 1) maximising the genetic relatedness between the reference population and selection candidates; 2) increasing the number of animals in the reference population; 3) ensuring the calibration phenotype is the most accurate possible (ie. increasing the heritability of the phenotype eg via appropriate test duration); or a combination of these factors.

The inclusion of a phenotypic indicator trait measured on all selection candidates was modelled on a reasonably optimistic scenario. However, while inclusion of RFI into the breeding programme via this mechanism generated positive returns, the benefits were small relative to the genomic selection scenarios while the costs were significantly larger. Thus to generate a better return than genomic selection, a phenotypic indicator would have to have a combination of parameters which here better than those used in this study. Given the practical considerations around implementation, the requirement for an additional measure to be adopted (vs no additional measurement in ram breeding flocks once genotyping is adopted), the unknown correlated responses in other traits to selection (this analysis assumed no correlated traits), and the R&D risk around identifying such a predictor, the outcomes suggest that further R&D investment would be best directed to improving genomic selection rather than a search for phenotypic predictors.

Table 3. Response to selection (cents/ewe/year), industry benefit and cost (\$M over benefit/cost horizons) by RFI genetic improvement scenario

Scenario	Base	Base+G	Base+G_R	Base+G_P	Base+G_RP	Base+N	Base+NG
Total Response	161.64	173.64	181.40	176.53	183.81	165.22	176.91
Relative to Base		12.0	19.8	14.9	22.2	3.6	15.3
Relative to Base + G			7.8	2.9	10.2	NA	3.3
Total benefit	947.0	993.2	1023.1	1004.4	1032.4	960.8	1005.8
Relative to Base		46.2	76.2	57.4	85.5	13.8	58.9
Relative to Base+G			29.9	11.2	39.2	NA	12.6
Cost Relative to Base – 100% of rams tested		13.3	14.2	13.8	14.7	4.4	17.8
Cost attributable to RFI – 100% of rams tested ¹			0.9	0.5	1.4	4.4	4.4

¹ For Base+G_R, Base+G_P, and Base+G_RP scenarios, the costs attributable to RFI are independent of the percentage of rams tested, whereas for Base+N/G, the costs scale up proportionally; 100% of rams are assumed to be phenotyped for the new selection criteria in the Base+N/G scenarios.

REFERENCES

Daetwyler, H.D., CALUS, M.P.L., PONG-WONG, R., DE LOS CAMPOS, G., Hickey, J.M. 2013 *Genetics* 193:347-365.